

FIGURE 1

1
ATGGCTCCCTTAGCCGAAGTCGGGGGCTTCTGGGCGGCCTGGAG
MetAlaProLeuAlaGluValGlyGlyPheLeuGlyGlyLeuGlu
46
GGCTTGGGCCAGCAGGTGGGTTCGCATTTCTGTTGCCTCCTGCC
GlyLeuGlyGlnGlnValGlySerHisPheLeuLeuProProAla
91
GGGAGCGGCCCGCTGCTGGGCGAGCGCAGGAGCGCGCGGAG
GlyGluArgProProLeuLeuGlyGluArgArgSerAlaAlaGlu
136
CGGAGCGCGCGCGGGCGGGGCTGCGCAGCTGGCGCACCTG
ArgSerAlaArgGlyGlyProGlyAlaAlaGlnLeuAlaHisLeu
181
CACGGCATCCTGCGCCGCCGGCAGCTCTATTGCCGCACCGGCTTC
HisGlyIleLeuArgArgArgGlnLeuTyrCysArgThrGlyPhe
226
CACCTGCAGATCCTGCCCCACGGCAGCGTGCAGGGCACCCGGCAG
HisLeuGlnIleLeuProAspGlySerValGlnGlyThrArgGln
271
GACCACAGCCTCTTCGGTATCTTGAATTCATCAGTGTGGCAGTG
AspHisSerLeuPheGlyIleLeuGluPheIleSerValAlaVal
316
GGA CTGGTCAGTATTAGAGGTGTGGACAGTGGTCTCTATCTTGA
GlyLeuValSerIleArgGlyValAspSerGlyLeuTyrLeuGly
361
ATGAATGACAAAGGAGAACTCTATGGATCAGAGAACTTACTTCC
MetAsnAspLysGlyGluLeuTyrGlySerGluLysLeuThrSer
406
GAATGCATCTTTAGGGAGCAGTTTGAAGAGAACTGGTATAACACC
GluCysIlePheArgGluGlnPheGluGluAsnTrpTyrAsnThr
451
TATTCATCTAACATATATAAACATGGAGAACTGGCCGCAGGTAT
TyrSerSerAsnIleTyrLysHisGlyAspThrGlyArgArgTyr
496
TTTGTGGCACTTAACAAAGACGGAAGTCCAAGAGATGGCGCCAGG
PheValAlaLeuAsnLysAspGlyThrProArgAspGlyAlaArg
541
TCCAAGAGGCATCAGAAAATTTACACATTTCTTACCTAGACCAGTG
SerLysArgHisGlnLysPheThrHisPheLeuProArgProVal
586
GATCCAGAAAGAGTTCCAGAATTGTACAAGGACCTACTGATGTAC
AspProGluArgValProGluLeuTyrLysAspLeuLeuMetTyr
631
ACT
Thr

```
Query:      170 TGGCGCACCTGCACGGCATCCTGCGCCGCCAGGCTCTATTGCCGCACCCGGCTTCCACC 229
           ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:       2 TGGATCATTAAAGGGGATTCTCAGGCGGAGGCAGCTATACTGCAGGACTGGATTTCAC 61

Query:     230 TGCAGATCCTGCCCGACGGCAGCGTG CAGGGCACCCGGCAGGACCACAGCCTCTTCGGTA 289
           | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     62 TAGAAATCTTCCCCAATGGTACTATCCAGGGAACCAGGAAAGACCACAGCCGATTGGCA 121

Query:     290 TCTTGGAATTCATCAGTGTGGCAGTGGGACTGGTCAGTATTAGAGGTGTGGACAGTGGTC 349
           | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:    122 TTCTGGAATTTATCAGTATAGCAGTGGGCCTGGTCAGCATTTCGAGGCGTGGACAGTGGAC 181

Query:     350 TCTATCTTGAATGAATGACAAAGGAGAACTCTATGGATCAGAGAACTTACTTCCGAAT 409
           |||| | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:    182 TCTACCTCGGGATGAATGAGAAGGGGGAGCTGTATGGATCAGAAAACTAACCCAAGAGT 241

Query:     410 GCATCTTTAGGGAGCAGTTTGAAGAGAACTGGTATAACACCTATTCATCTAACATATATA 469
           | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:    242 GTGTATTTCAGAGAACAGTTCGAAGAAAACCTGGTATAATACGTACTCGTCAAACCTATATA 301

Query:     470 AACATGGAGACACTGGCCGCAGGTATTTTGTGGCACTTAACAAAGACGGAACCTCCAAGAG 529
           | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:    302 AGCACGTGGACACTGGAAGGCGATACTATGTTGCATTAAATAAAGATGGGACCCCGAGAG 361

Query:     530 ATGGCGCCAGGTCCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCAGTGGATC 589
           | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:    362 AAGGGACTAGGACTAAACGGCACCAGAAATTCACACATTTTTTACCTAGACCAGTGGACC 421

Query:     590 CAGA 593
           |||
Sbjct:    422 CCGA 425
```

FIGURE 3

>gb:GenBank accession number -ID:AB020858|acc:AB020858 Homo sapiens genomic DNA of p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 1/11 - Homo sapiens, 100000 bp.

Minus Strand HSPs:

A.

Score = 1430 (214.6 bits), Expect = 1.6e-126, Sum P(3) = 1.6e-126
Identities = 288/289 (99%), Positives = 288/289 (99%),
Strand = Minus / Plus

```
Query:   289 TACCGAAGAGGCTGTGGTCTCTGCCGGGTGCCCTGCACGCTGCCGTCGGGCAGGATCTGCA 230
          |||
Sbjct: 15927 TACCGAAGAGGCTGTGGTCTCTGCCGGGTGCCCTGCACGCTGCCGTCGGGCAGGATCTGCA 15986

Query:   229 GGTGGAAGCCGGTGC CGGCAATAGAGCTGCCGGCGGCGCAGGATGCCGTGCAGGTGCGCCA 170
          |||
Sbjct: 15987 GGTGGAAGCCGGTGC CGGCAATAGAGCTGCCGGCG- CGCAGGATGCCGTGCAGGTGCGCCA 16045

Query:   169 GCTGCGCAGCCCCCGGCCGCGCGCGCTCCGCTCCGCGCGCTCCTGCGCTCGCCCA 110
          |||
Sbjct: 16046 GCTGCGCAGCCCCCGGCCGCGCGCGCTCCGCTCCGCGCGCTCCTGCGCTCGCCCA 16105

Query:   109 GCAGCGGCGGCGCTCCCCGGCAGGAGGCAACAGGAAATGCGAACCCACCTGCTGGCCCA 50
          |||
Sbjct: 16106 GCAGCGGCGGCGCTCCCCGGCAGGAGGCAACAGGAAATGCGAACCCACCTGCTGGCCCA 16165

Query:    49 AGCCCTCCAGGCCGCCCAGAAAGCCCCCGACTTCGGCTAAGGGAGCCAT 1
          |||
Sbjct: 16166 AGCCCTCCAGGCCGCCCAGAAAGCCCCCGACTTCGGCTAAGGGAGCCAT 16214
```

B.

Score = 1224 (183.6 bits), Expect = 1.6e-126, Sum P(3) = 1.6e-126
Identities = 250/255 (98%), Positives = 250/255 (98%),
Strand = Minus / Plus

```
Query:   633 AGTGATACATCAGTAGGTCCTTGTAACAATTCTGGAACCTCTTTCTGGATCCACTGGTCTAGG 574
          |||
Sbjct: 7257 AGTGATACATCAGTAGGTCCTTGTAACAATTCTGGAACCTCTTTCTGGATCCACTGGTCTAGG 7316

Query:   573 TAAGAAATGTGTAAATTTCTGATGCCTCTTGGACCTGGCGCCATCTCTTGGAGTTCCGTC 514
          |||
Sbjct: 7317 TAAGAAATGTGTAAATTTCTGATGCCTCTTGGACCTGGCGCCATCTCTTGGAGTTCCGTC 7376

Query:   513 TTTGTTAAGTGCCACAAAATACCTGCGGCCAGTGTCTCCATGTTTATATATGTTAGATGA 454
          |||
Sbjct: 7377 TTTGTTAAGTGCCACAAAATACCTGCGGCCAGTGTCTCCATGTTTATATATGTTAGATGA 7436

Query:   453 ATAGGTGTTATACAGTTCTCTTCAAAGTCTCCCTAAAGATGCATTGGAAGTAAGTTT 394
          |||
Sbjct: 7437 ATAGGTGTTATACAGTTCTCTTCAAAGTCTCCCTAAAGATGCATTGGAAGTAAGTTT 7496
```

C.

```

Query:      391 CTGATCCATAGAGTTCTCCTTTGTCAATTCATTCCAAGATAGAGACCACTGTCCACACCTC 332
             |||
Sbjct:     9837 CTGATCCATAGAGTTCTCCTTTGTCAATTCATTCCAAGATAGAGACCACTGTCCACACCTC 9896

Query:      331 TAATACTGACCAGTCCCACTGCCACACTGATGAATTCCAAGATACC 286
             |||
Sbjct:     9897 TAATACTGACCAGTCCCACTGCCACACTGATGAATTCCAAGATACC 9942

```

FIGURE 4

Sequences analyzed:

1. HUMAN FGF-9 (P31371_HUMAN FGF-9) [SEQ ID NO:9]
2. MOUSE FGF-9 (P54130_MOUSE FGF-9) [SEQ ID NO:10]
3. RAT FGF-9 (P36364_FGF9_RAT FGF-9) [SEQ ID NO:11]
4. XENOPUS XFGF-CX (BAA83474Xen; Xenopus laevis XFGF-CX) [SEQ ID NO:12]
5. FGF-CX (cgAB020858) [SEQ ID NO:2]

Multiple Alignment:

HUMAN FGF-9
RAT FGF-9
MOUSE FGF-9
XENOPUS XFGF-CX
FGF-CX

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M A P L G E V G N Y F G V Q D A V P - - F G N V P V L P - - V D S P V L L S D H L G Q S E A G G L P R G P A V T D L D H
M A P L G E V G S Y F G V Q D A V P - - F G N V P V L P - - V D S P V L L S D H L G Q S E A G G L P R G P A V T D L D H
M A P L G E V G S Y F G V Q D A V P - - F G N V P V L P - - V D S P V L L N D H L G Q S E A G G L P R G P A V T D L D H
M A P L A D V G T F L G G Y D A T G - Q V G S H F F L L P P A K D S P L L F N D P L A Q Q S E R L S R - S T P - S D L S H
M A P L A E V G G F L G G L E G L G Q Q V G S H F F L L P P A G E R P P L L G R R S A A E R S A R - G G P C A A Q L A H

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HUMAN FGF-9
RAT FGF-9
MOUSE FGF-9
XENOPUS XFGF-CX
FGF-CX

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L K G I L R R R Q L Y C R T G F H L E I F P N G T I Q G T R K D H S R F G I L E F I S I A V G L V S I R G V D S G L Y L
L K G I L R R R Q L Y C R T G F H L E I F P N G T I Q G T R K D H S R F G I L E F I S I A V G L V S I R G V D S G L Y L
L K G I L R R R Q L Y C R T G F H L E I F P N G T I Q G T R K D H S R F G I L E F I S I A V G L V S I R G V D S G L Y L
L Q G I L R R R Q L Y C R T G F H L Q I L P D G N V Q G T R Q D H S R F G I L E F I S V A G L V S I R G V D S G L Y L
L H G I L R R R Q L Y C R T G F H L Q I L P D G S V Q G T R Q D H S R F G I L E F I S V A G L V S I R G V D S G L Y L

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HUMAN FGF-9
RAT FGF-9
MOUSE FGF-9
XENOPUS XFGF-CX
FGF-CX

```

G M N E K G E L Y G S E K L T Q E C V F R E Q F E E N W Y N T Y S S N L Y K H V D T G R R Y Y V A L N K D G T P R E G T
G M N E K G E L Y G S E K L T Q E C V F R E Q F E E N W Y N T Y S S N L Y K H V D T G R R Y Y V A L N K D G T P R E G T
G M N E K G E L Y G S E K L T Q E C V F R E Q F E E N W Y N T Y S S N L Y K H V D T G R R Y Y V A L N K D G T P R E G T
G M N E K G E L Y G S E K L T S E C I F R E Q F E E N W Y N T Y S S N L Y K H G D S G R R Y Y V A L N K D G T P R E G T
G M N E K G E L Y G S E K L T S E C I F R E Q F E E N W Y N T Y S S N L Y K H G D I G R R Y Y V A L N K D G T P R E G T

```

HUMAN FGF-9
RAT FGF-9
MOUSE FGF-9
XENOPUS XFGF-CX
FGF-CX

```

R T K R H Q K F T H F L P R P V D P D K V P E L Y K D I L S Q S
R T K R H Q K F T H F L P R P V D P D K V P E L Y K D I L S Q S
R T K R H Q K F T H F L P R P V D P D K V P E L Y K D I L S Q S
R A K R H Q K F T H F L P R P V D P E K V P E L Y K D L M G Y S
R S K R H Q K F T H F L P R P V D P E R V P E L Y K D L L M Y T

```

FIGURE 5

FGF-CX	MAPLAEVGGFLRGLEGLGQVQVSSHFLPPA GERPPLLGERSSAERSAR- GGPEAAQLAH	59
XFGF-20	MAPLAEVGTFELGGYDALG-QVSSHFLPPAKDSPLLENDPLAQSEELSE-SAP--SDLSH	56
FGF-9	MAPLGEVGNVFGVQDAWP--FENVPPLP--VDSFWLLSDHLGQSEAGGLPREPAVTDLDH	56
FGF-16	---MAEVGGVFA SLDWDLHGFS S LGNVPLADSPGFLNERLGQIEGKLQREGSP--TDFAH	55
FGF-CX	LHGILRRRQLYCRTGFHLQILPDGSGWQGTRODHSLEGFLEFISVAVGLVSIKGVDSGLYL	119
XFGF-20	LQSIILRRRQLYCRTGFHLQILPDGNWQGTRODHSRFGILEFISVAGLVSIRGVDLGLYL	116
FGF-9	LKGILRRRQLYCRTGFHLEIFPNGTQQGTREKDHRSRFGILEFISVAVGLVSIKGVDSGLYL	116
FGF-16	LKGILRRRQLYCRTGFHLEIFPNGTWHGTRHDHSRFGILEFISVAVGLSIRGVDSGLYL	115
FGF-CX	GMNDKGELYGSEKLTSECFREQFEENWYNTYSSNLYKHGDTGRRYFVALNKDGTPEDEA	179
XFGF-20	GMNDKGELGSEKLTSECFREQFEENWYNTYSSNLYKHGDSGRRYFVALNKDGTPEDEGT	176
FGF-9	GMNEKGELYGSEKLTQECVFREQFEENWYNTYSSNLYKHVDGRRYFVALNKDGTPEDEGT	176
FGF-16	GMNERGELYGSKKLTREGVFREQFEENWYNTYASTLYKHSLSERQYFVALNKDGSPEDEGY	175
FGF-CX	RSKRHQKFTTHFLPRPVDPERVPELYKDL LLMVY	211
XFGF-20	RAKRHQKFTTHFLPRPVDPEKVP ELYKDL LMGYS	208
FGF-9	RTKRHQKFTTHFLPRPVDPEKVP ELYKDL LLSQS	208
FGF-16	RTKRHQKFTTHFLPRPVDPSKLP S M S R D L F H Y R	207

FIGURE 6

p1nr:SWISSPROT-ACC:P31371 GLIA-ACTIVATING FACTOR PRECURSOR (GAF) (FIBROBLAST GROWTH FACTOR-9)
(FGF-9) (HBGF-9) - HOMO SAPIENS (HUMAN), 208 aa. Identities = 147/208 (70%), Positives = 170/208
(81%)

Query:	1	MAPLAEVGGFLGLEGLGQQVGSFLLPPAGERPPLLGERSSAAERSARG-GPGAAQLAH	59
Sbjct:	1	MAPLGEVGNVFGVQDAV--PFGNVPLPV--DSPVLLSDHLGQSEAGGLPRGPAVTDLDH	56
Query:	60	LHGILRRRLYCRITGFHLQILPDGSVQGTQDHSLEFISVAVGLVSIKGVDSGLYL	119
Sbjct:	57	LKGILRRRLYCRITGFHLQILPDGSVQGTQDHSLEFISVAVGLVSIKGVDSGLYL	116
Query:	120	GMNDKGELYGSEKLTSECFREQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA	179
Sbjct:	117	GMNEKGELYGSEKLTQECVFEQFEENWNTYSSNIYKHVDTGRRYVVALNKDGTREGT	176
Query:	180	RSKRHQKFTTHFLPRPVDPERVPELYKDLL	208
Sbjct:	177	RTKRHQKFTTHFLPRPVDPERVPELYKDIL	205

FIGURE 7

Length = 208

Plus Strand HSPs:

Score = 775 (272.8 bits), Expect = 3.4e-76, P = 3.4e-76
 Identities = 147/208 (70%), Positives = 170/208 (81%), Frame = +1

Query:	1	MAPLAEVGGFLGGLGQQVGSFLLPPAGERPPLLGERSSAAERSARG-GPGAAQLAH	59
Sbjct:	1	MAPLGEVGSYFGVQDAV--PFGNVPVLPV--DSPVLLNDHLGQSEAGGLPRGPAVTDLDH	56
Query:	60	LHGILRRRQLYCRTGFHLQILPDGSVQGTQDHSLFGILEFISVAVGLVSIRGVDSGLYL	119
Sbjct:	57	LKGILRRRQLYCRTGFHLEIFPNGTIQTRKDHRSFGILEFISIAVGLVSIRGVDSGLYL	116
Query:	120	GMNDKGELYGSEKLTSECIFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA	179
Sbjct:	117	GMNEKGELYGSEKLTQECVFRREQFEENWYNTYSSNLYKHVDTGRRYYVALNKDGTREGT	176
Query:	180	RSKRHQKFTHFLPRPVDPERVPELYKDIL	208
Sbjct:	177	RTKRHQKFTHFLPRPVDKVPPELYKDIL	205

Length = 208

Plus Strand HSPs:

Score = 775 (272.8 bits), Expect = 3.4e-76, P = 3.4e-76
Identities = 147/208 (70%), Positives = 170/208 (81%), Frame = +1

[illegible]

FIGURE 9

FGF-CX Query Length = 211
 XFGF-CX Sbjct Length = 208

Plus Strand HSPs:

Score = 906 (318.9 bits), Expect = 4.4e-90, P = 4.4e-90
 Identities = 170/211 (80%), Positives = 189/211 (89%), Frame = +1

Query:	1	MAPLAEVGGFLGGLGQQVGSFLLPPAGERPPLLGERSSAERSARGGPGAAQLAHL	60
		+ + + + + + +	
Sbjct:	1	MAPLADVGTFLGGYDALGQ-VGSFLLPPAKDSPLLFNDPLAQSERLSRSAP--SDLSHL	57
Query:	61	HGILRRRLYCRGTGFHLQILPDGVSQGTQDHSLSFGILEFISVAVGLVSIRGVDSGLYL	120
		+ +	
Sbjct:	58	QGILRRRLYCRGTGFHLQILPDGNVQGTQDHSRFGILEFISVAIGLVSIRGVDTGLYL	117
Query:	121	MNDKGELYGSEKLTSECIFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRD	180
		+ +	
Sbjct:	118	MNDKGELFGSEKLTSECIFREQFEENWYNTYSSNLKKGDSGRRYFVALNKDGTPRD	177
Query:	181	SKRHQKFTHFLPRPVDPERVPELYKDILLMYT	211
		+ + + +	
Sbjct:	178	AKRHQKFTHFLPRPVDPEKVPPELYKDLMGYS	208

FIGURE 10

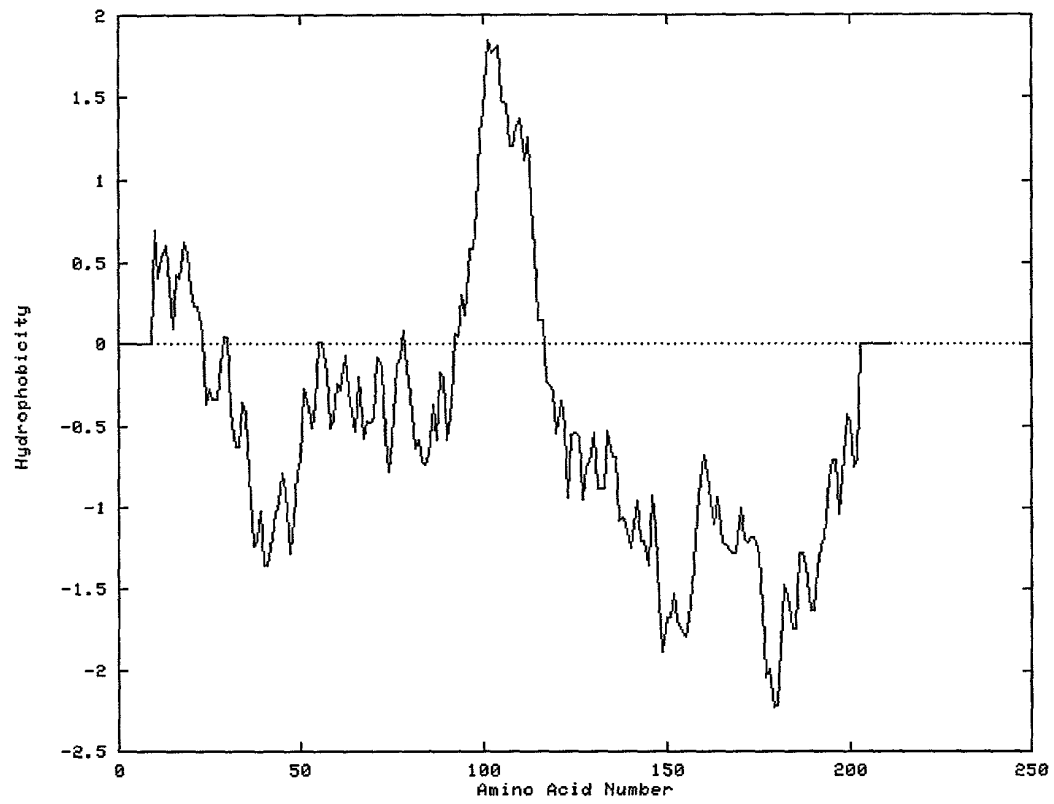


FIGURE 11

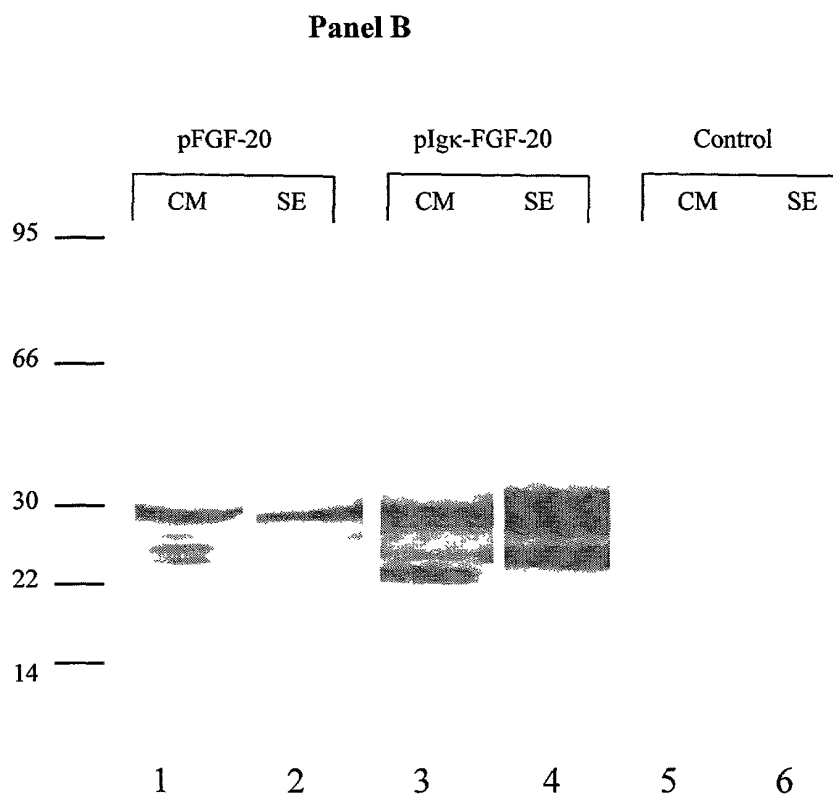
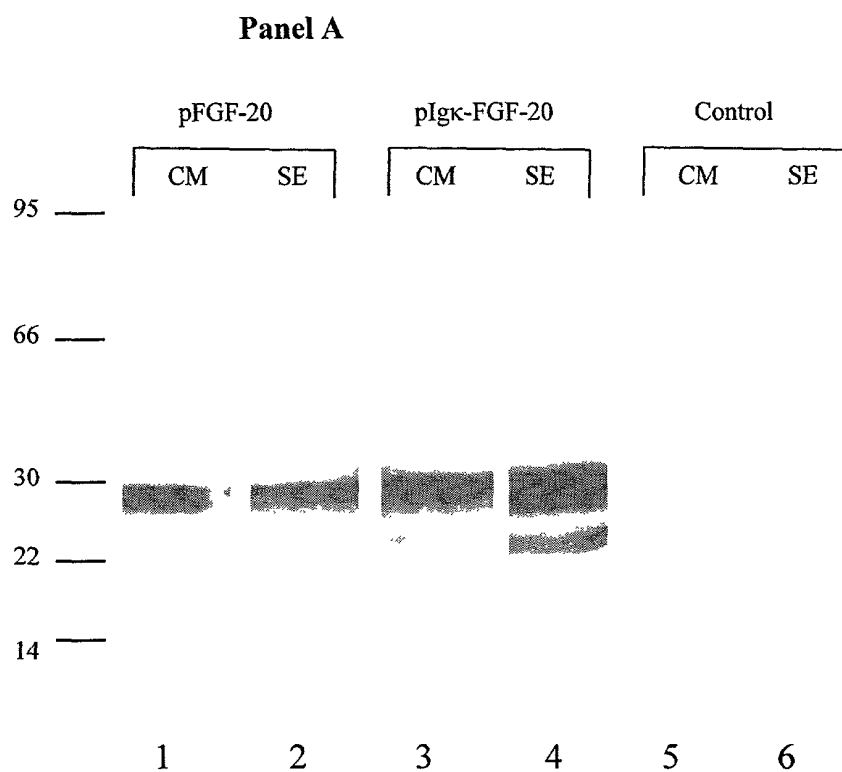


FIGURE 12.

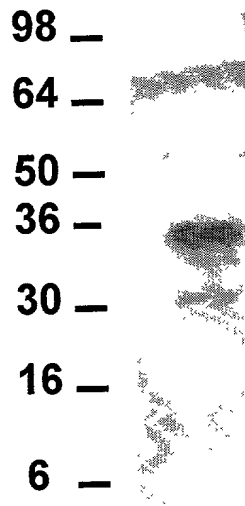


Figure 13.

Exon 1
 ...AGACAGTGAGAGCTTCCCTGCCATTTCAGTGCAAAGTCCCTCCGGAGCGACCTCAGAGGAGTAACCGGCGCTTAACT
 TTTTGGCGCTCGTTTGTCTATAATTTTCTCTATCCACCTCCACCCCAACACTCTTTACTGGGGGGTCTTTT
 GTGTTCCGGATCTCCCCCTCCATGGCTCCCTTAGCCGAAGTCGGGGGCTTTCTGGGGCGCCTGGAGGGCTTGGGCCAGCA
 1 M A P L A E V G G F L G G L E G L G Q Q
 21 GGTGGTTTCGCAATTCCTGTTCCTCCTGCCGGGAGCGCGCGCTGTGGCGAGCGCAGGAGCGGGCGGAGCGGA
 V G S H F L L P P A G E R P P L L G E R R S A A E R S
 48 GCGCGCGGGCGGGGCTGCGCAGCTGCGCACCTGCGCATCCTGCGCGCGGAGCTCTATTGCCGCACC
 A R G G P G A A Q L A H L H G I L R R R Q L Y C R T
 <-|-> Exon 2
 74 GGTTCCACCTGCAGATCCTGCCCGACCGGCAGCGTGCAGGGCACCCGCGCAGGACCCACAGCCTCTTCGGTATCTTGGAAAT
 G F H L Q I L P D G S V Q G T R Q D H S L F G I L E F
 CATCAGTGTGGCAGTGGGACTGGTCAGTATTAGAGGTGTGGACAGTGGTCTCTATCTTGGATGAATGACAAAGGAGAAC
 101 I S V A V G L V S I R G V D S G L Y L G M N D K G E L
 <-|-> Exon 3
 128 TCTATGGATCAGAGAAACTTACTTCCGAATGCATCTTTAGGGAGCAGTTTGAAGAGAACTGGTATAACACCTATTTCATCT
 Y G S E K L T S E C I F R E Q F E E N W Y N T Y S S
 AACATATATAACATGGAGACACTGGCCGCGAGGTATTTGTGGCACTTAACAAAGACGGAACCTCCAAGAGATGGCGCCAG
 154 N I Y K H G D T G R R Y F V A L N K D G T P R D G A R
 GTCCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCAGTGGATCCAGAAAGAGTTCCAGAATTGTACAAGACC
 181 S K R H Q K F T H F L P R P V D P E R V P E L Y K D L
 TACTGATGTACACTGA...
 208 L M Y T

Figure 14.

98—
64—
50—
36—
30—
16—
6 —

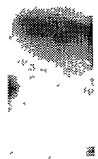


Figure 15, Panel A.

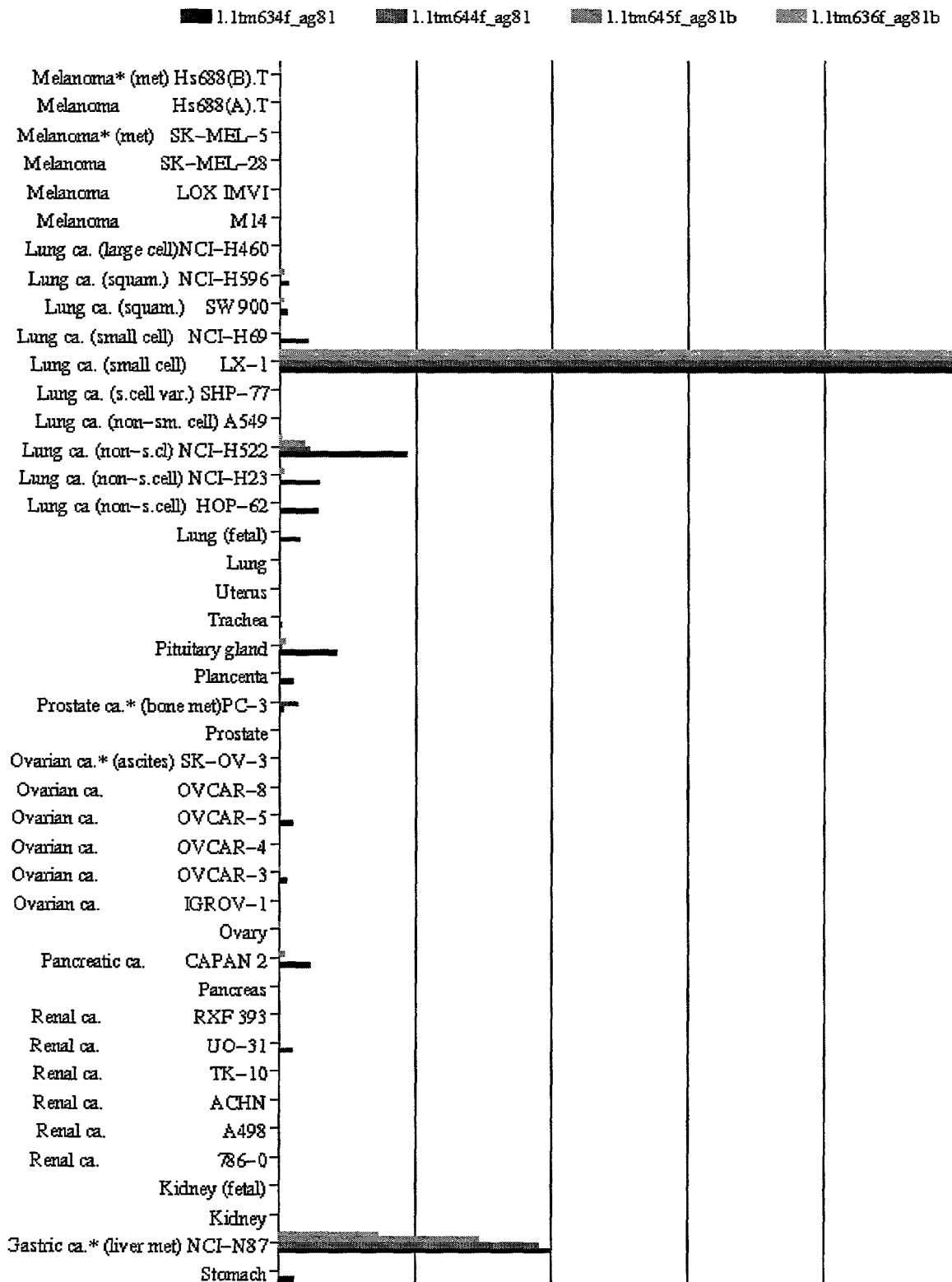


Figure 15, Panel B.

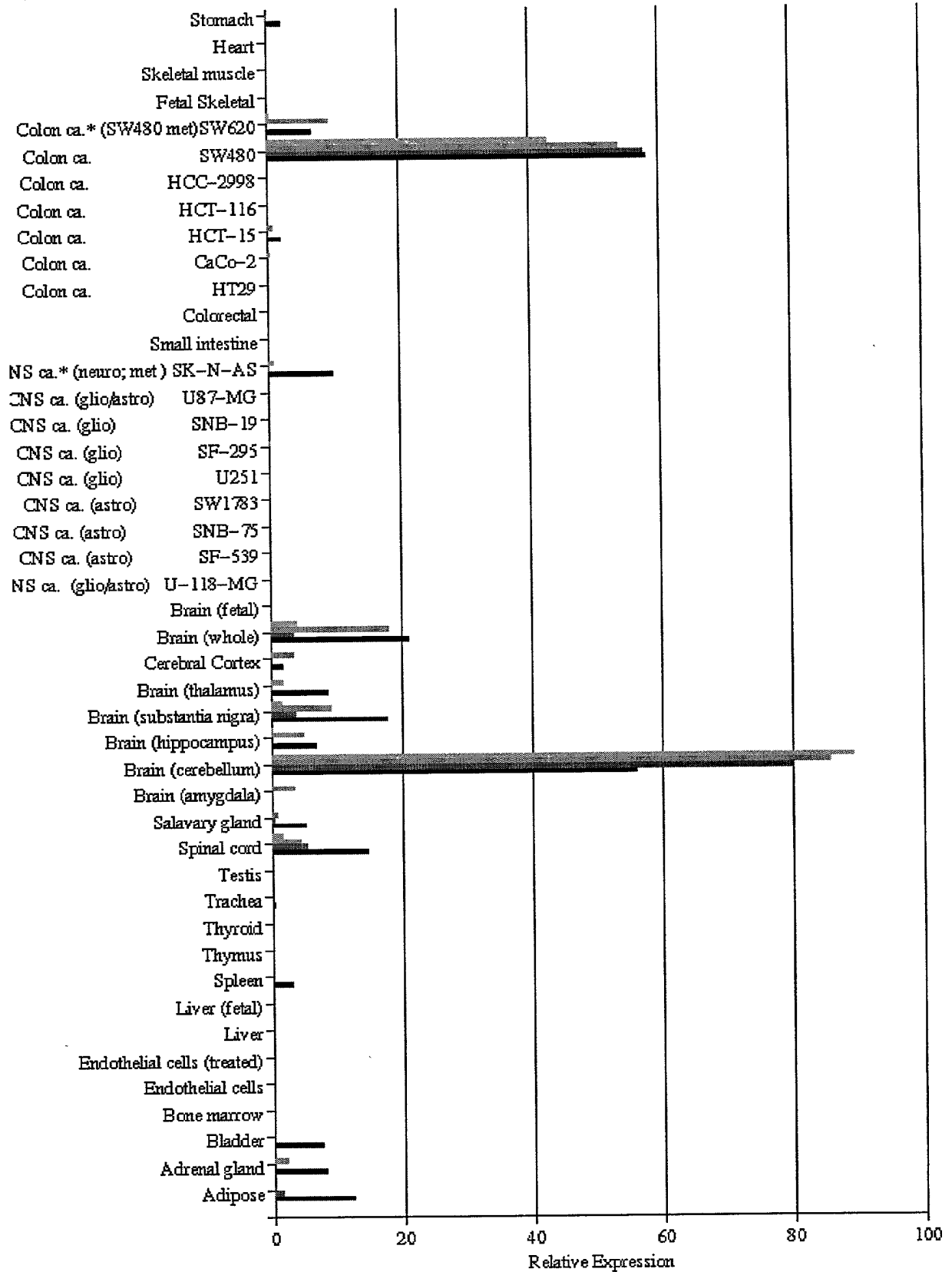


Figure 15, Panel C.

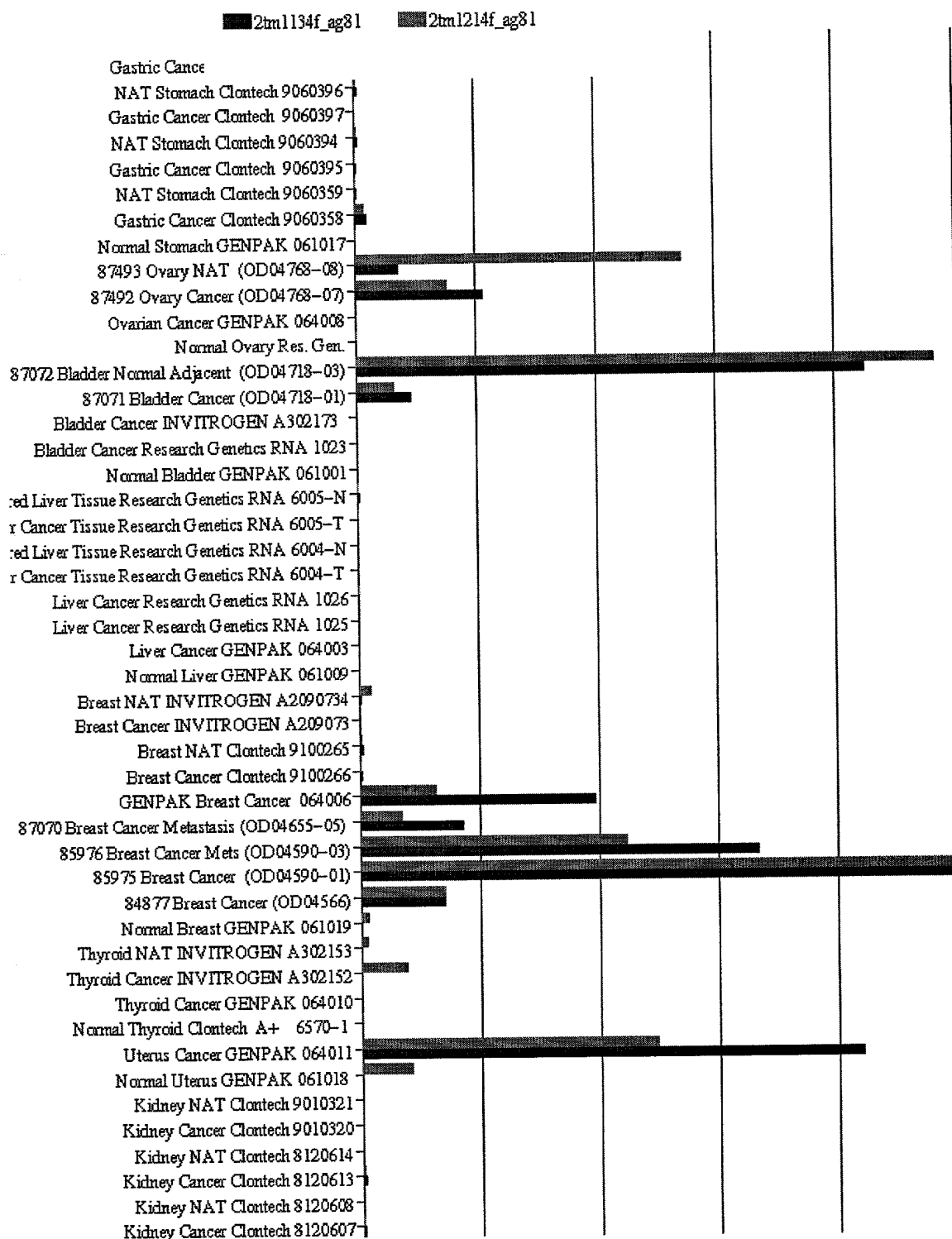


Figure 15, Panel D.

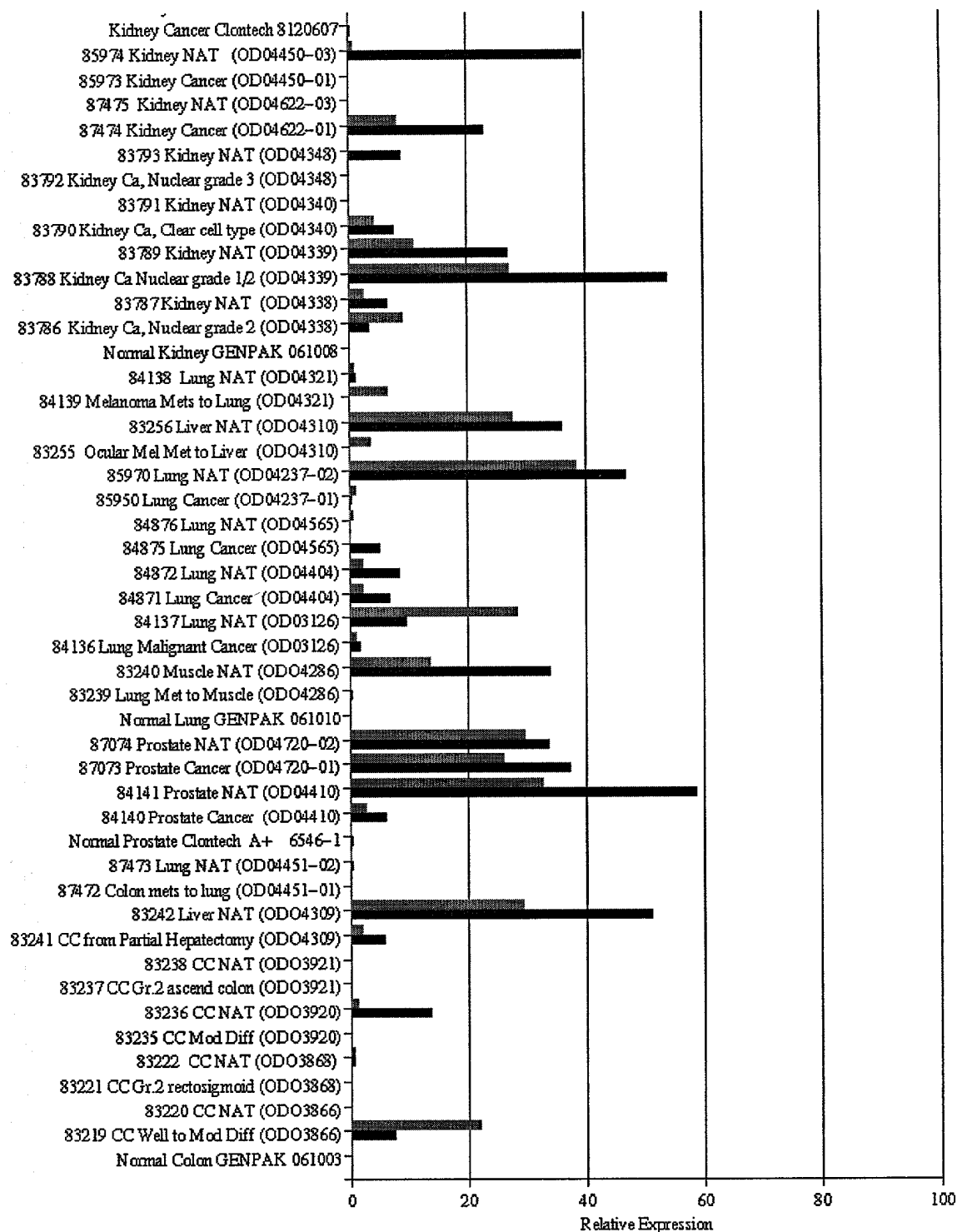


FIGURE 16.

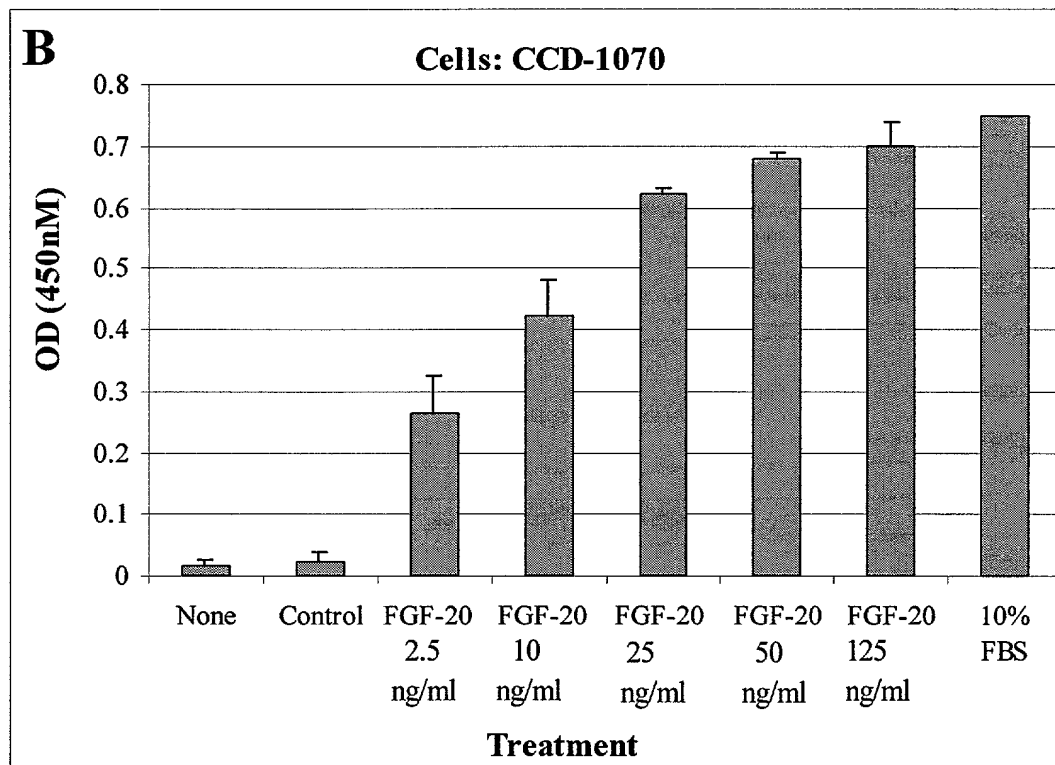
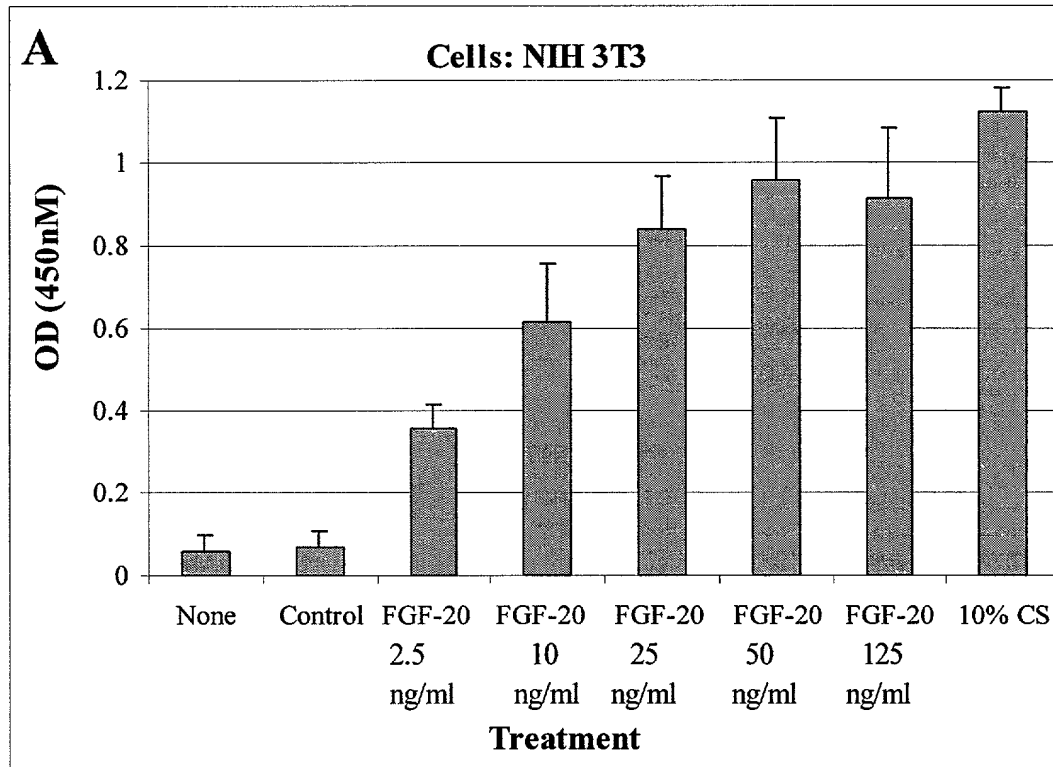


FIGURE 16 (continued).

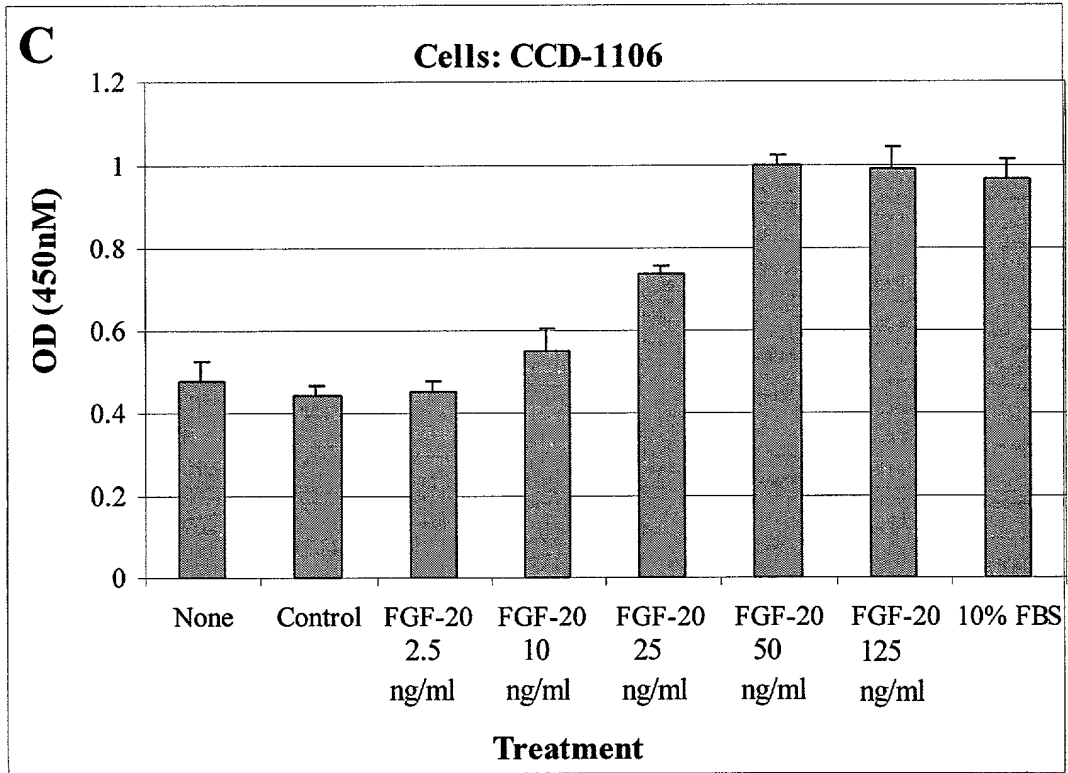


FIGURE 17.

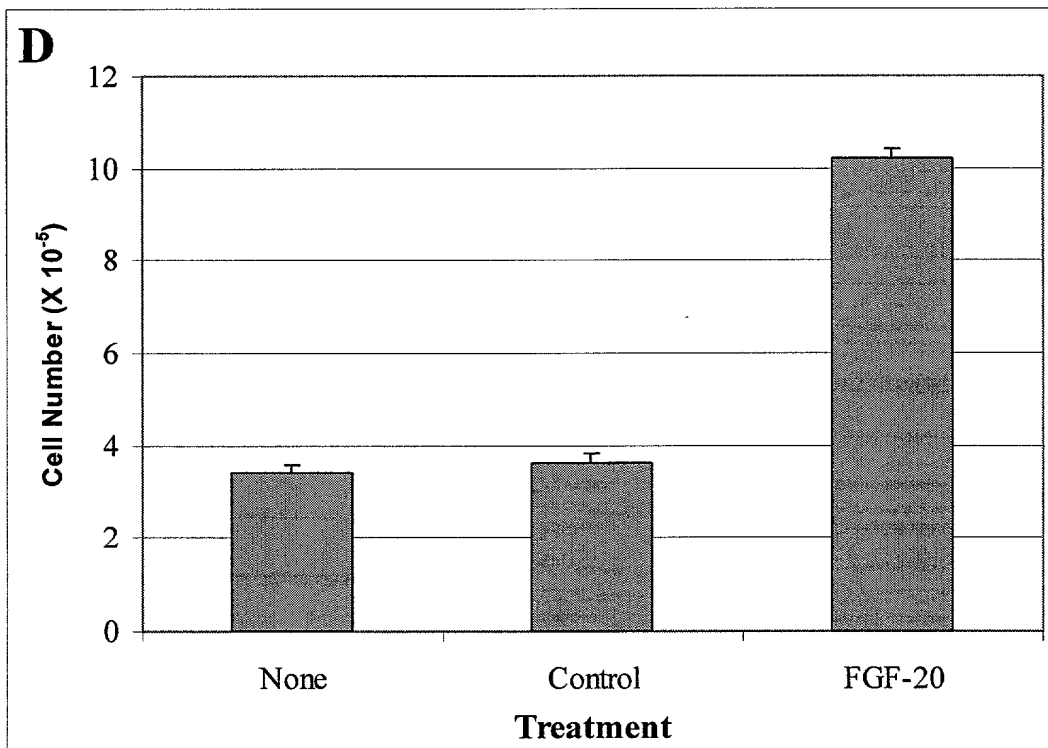


FIGURE 18.

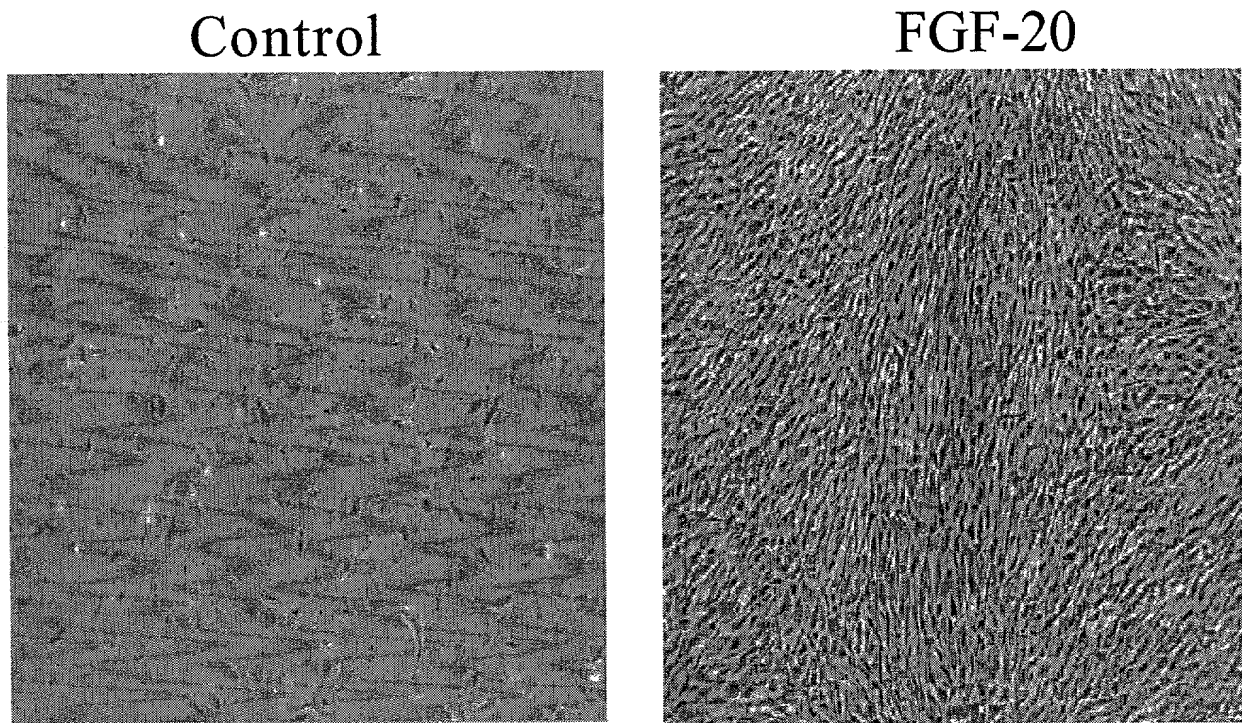


FIGURE 19.

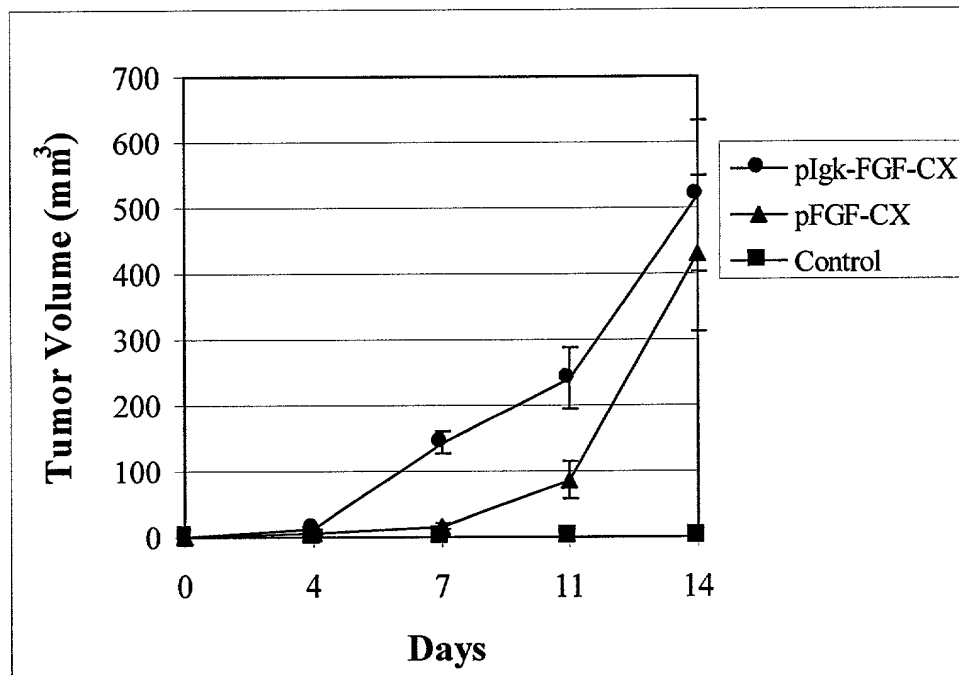


FIGURE 20.

Control



CG-AB020858

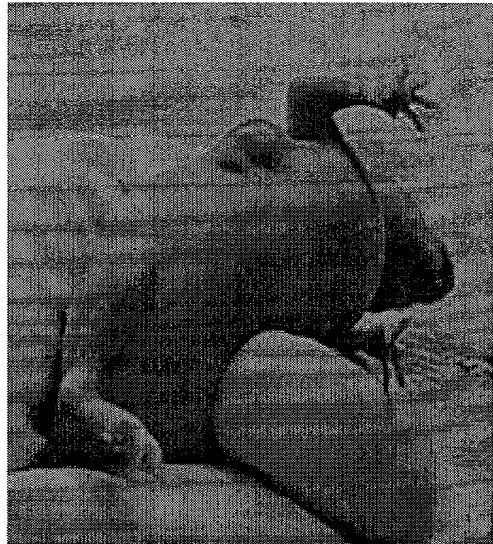


FIGURE 21.

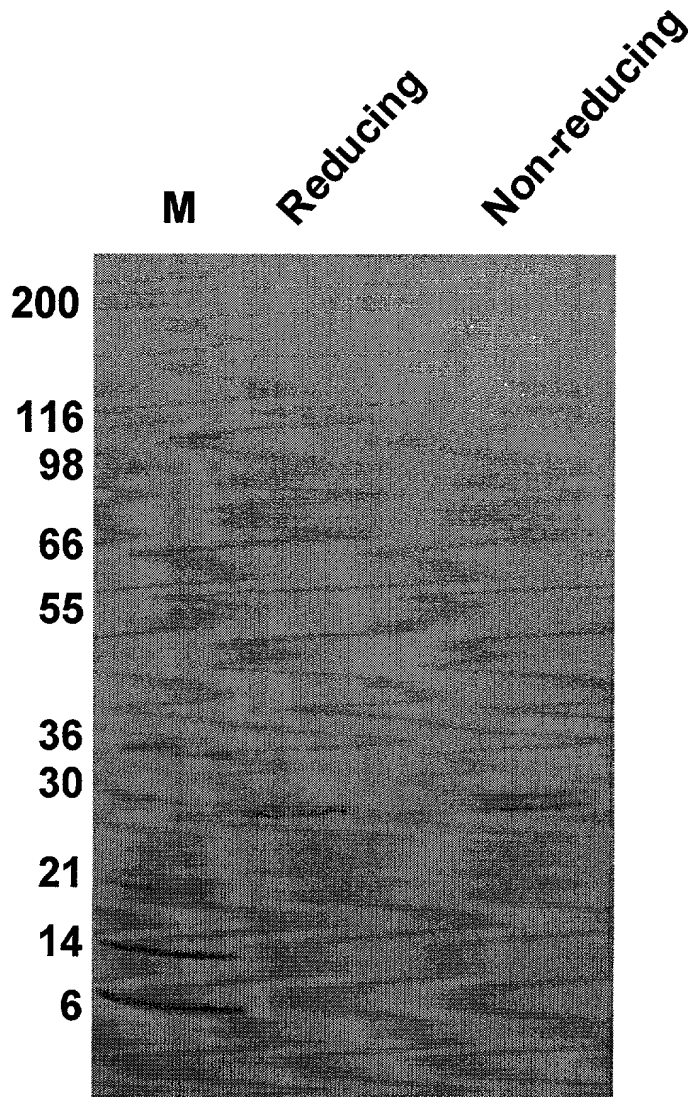


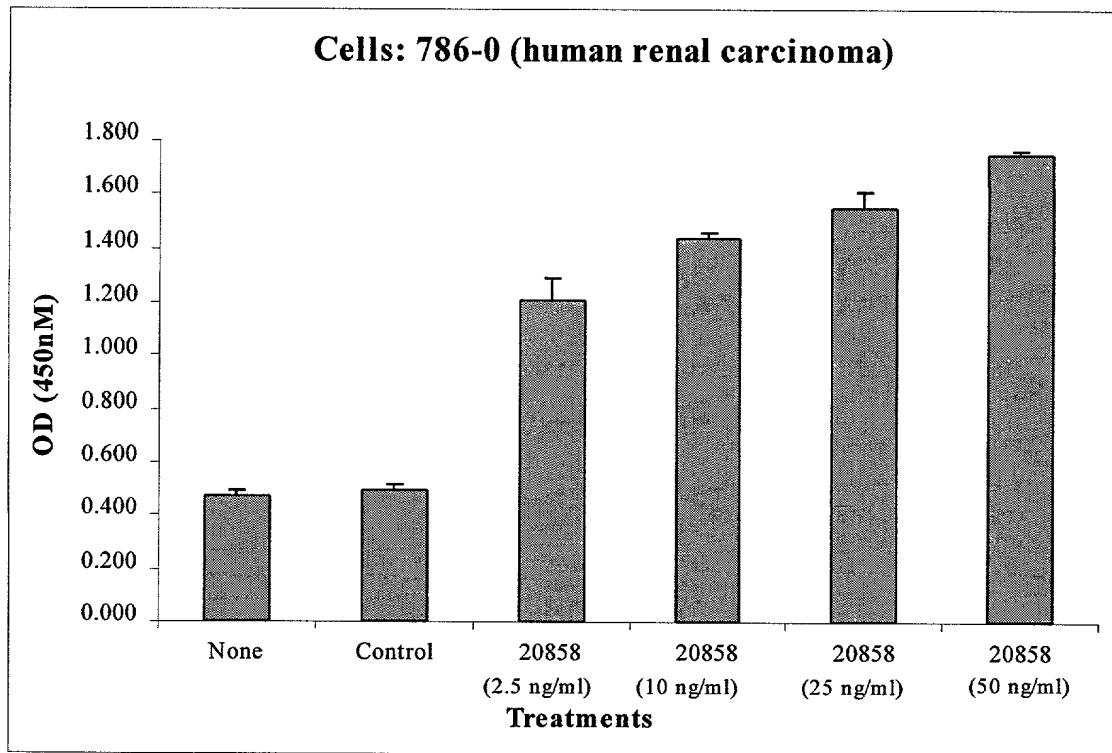
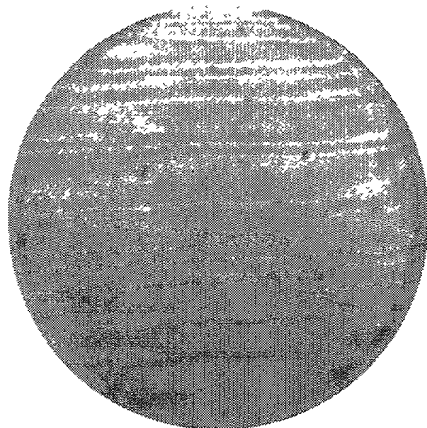
FIGURE 22.

FIGURE 23.

Control



pFGF-20



pIgk-FGF-20

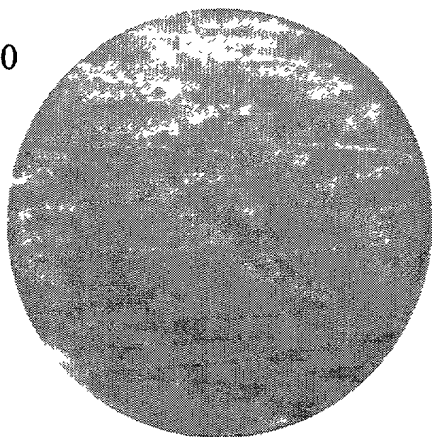


FIGURE 24

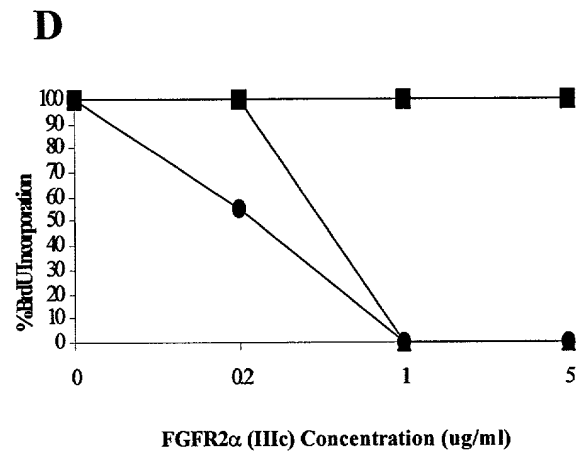
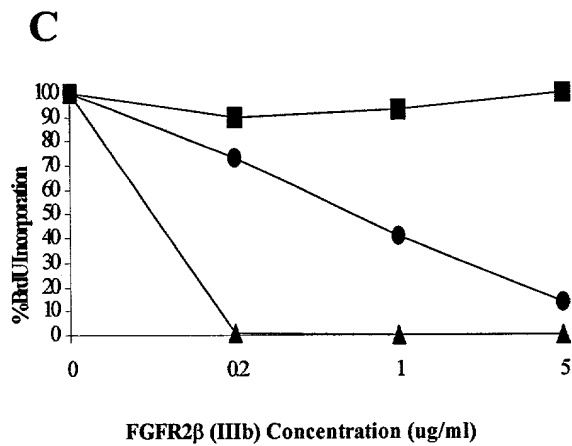
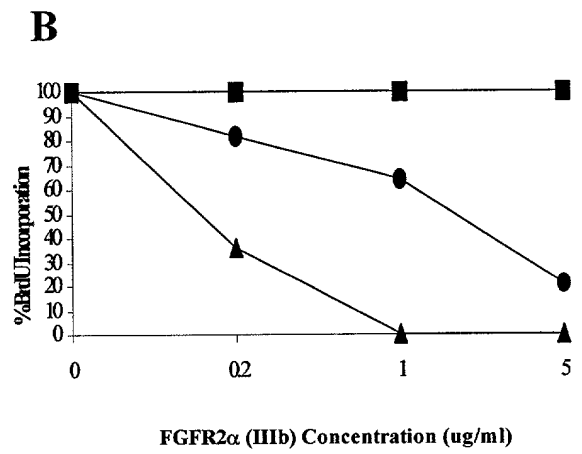
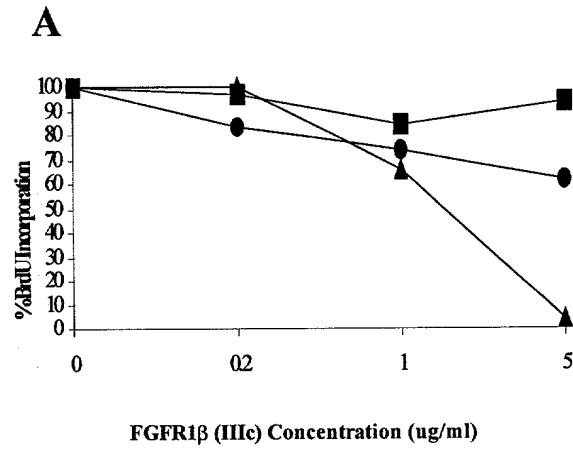


FIGURE 24 (ctd)

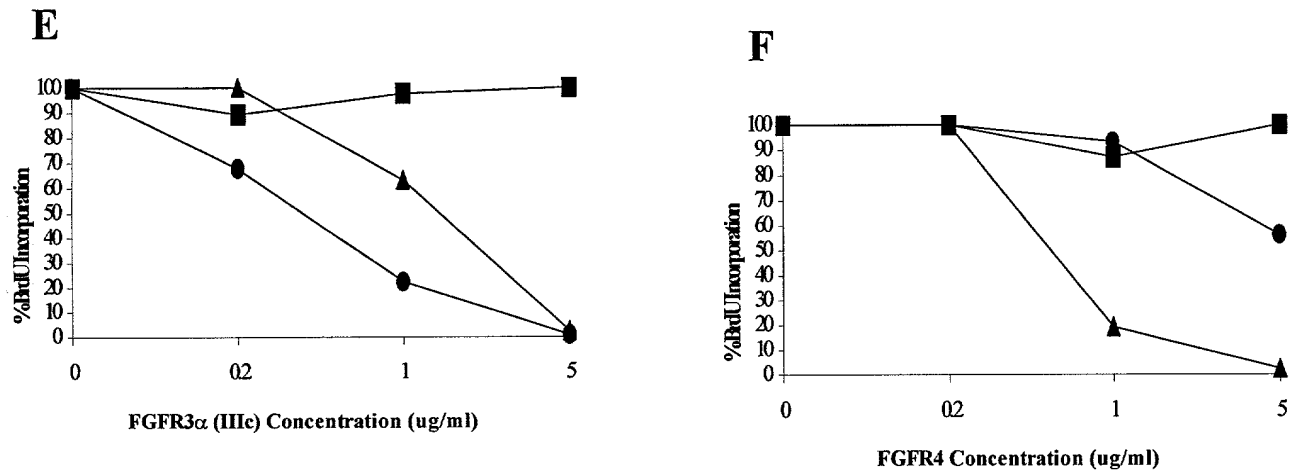


FIGURE 25

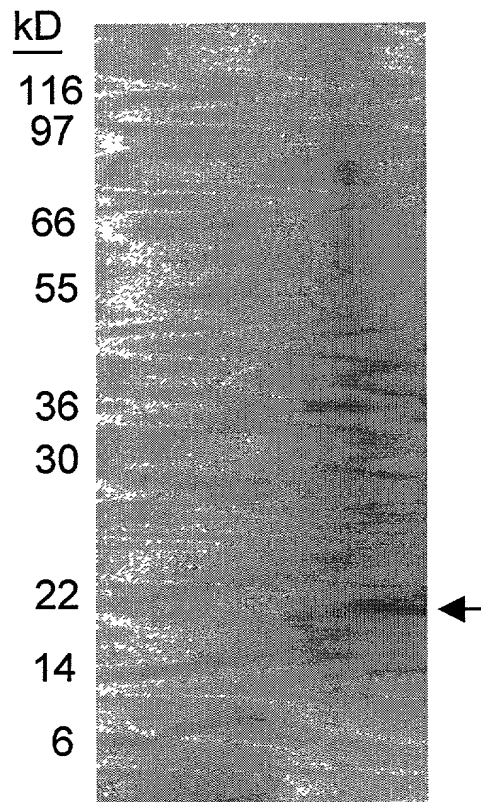


FIGURE 26

